

**AMENDMENTS TO THE SPECIFICATION**

*Please replace the previously submitted sequence listing with the replacement sequence listing submitted herewith.*

*Please replace the paragraph beginning at page 2, line 6, with the following rewritten paragraph:*

A prokaryotic DNA repair ligase polypeptide may comprise an amino acid sequence from a prokaryotic cell which shares greater than about 20% sequence identity with the sequence of Mt-Lig (CAB08492; SEQ ID NO: 91), greater than about 30%, greater than about 40%, greater than about 50%, greater than about 60%, greater than about 70%, greater than about 80%, greater than about 90% or greater than about 95% with the given amino acid sequence.

*Please replace the paragraphs beginning at page 2, line 18, with the following rewritten paragraphs:*

A primase domain may share greater than about 20% sequence identity with the sequence of Mt-Lig (CAB08492; SEQ ID NO: 91) between residues 1-324, greater than about 30%, greater than about 40%, greater than about 50%, greater than about 60%, greater than about 70%, greater than about 80%, greater than about 90% or greater than about 95% with the given amino acid sequence.

A nuclease domain may share greater than about 20% sequence identity with the sequence of Mt-Lig (CAB08492; SEQ ID NO: 91) between residues 325-447, greater than about 30%, greater than about 40%, greater than about 50%, greater than about 60%, greater than about 70%, greater than about 80%, greater than about 90% or greater than about 95% with the given amino acid sequence.

A ligase domain may share greater than about 20% sequence identity with the sequence of Mt-Lig (CAB08492; SEQ ID NO: 91) between residues 448-759, greater than about 30%, greater than about 40%, greater than about 50%, greater than about 60%, greater than about 70%, greater than about 80%, greater than about 90% or greater than about 95% with the given amino acid sequence.

*Please replace the paragraph beginning at page 3, line 15, with the following rewritten paragraph:*

In some preferred embodiments, the prokaryotic DNA repair ligase polypeptide is an Mt-lig polypeptide. An Mt-lig polypeptide may comprise or consist of the amino acid sequence of database accession number CAB08492 (SEQ ID NO: 91), which is encoded by the M. tuberculosis ORF RV0938 (Z95209) or may be a variant or allele of this sequence.

*Please replace the paragraph beginning at page 3, line 29, with the following rewritten paragraph:*

A prokaryotic Ku polypeptide may comprise an amino acid sequence from a prokaryotic cell which shares greater than about 20% sequence identity with the sequence of Mt-Ku (CAB08491; SEQ ID NO: 92), greater than about 30%, greater than about 40%, greater than about 50%, greater than about 60%, greater than about 70%, greater than about 80%, greater than about 90% or greater than about 95% with the given amino acid sequence.

*Please replace the paragraph beginning at page 4, line 5, with the following rewritten paragraph:*

In preferred embodiments, the prokaryotic Ku polypeptide is an Mt-Ku polypeptide. An Mt-Ku polypeptide may comprise or consist of the amino acid sequence of database accession number CAB08491 (SEQ ID NO: 92) that is encoded by the M. tuberculosis ORF RV0937c (Z95209) or may be a variant or allele of this sequence.